

APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS 530 387.1

FIGURE 1

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGAGGCCACACCAGGACTGT
 GTTGAAGGGTGTCCCCCTAAATGTAATACCTCCTCATCTTCTTACACAGTG
 TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA
 CTACTCTCTGACAGTCCTAGACTGGTCTTACACTAACAGACACC**ATGAAGGAGTATGTG**
 CTCCTATTATTCTGGCTTGTGCTGCCAACCTCTTAGCCCTCACACATCGCACT
 GAAGAACATGATGCTGAAGGATATGGAAGAACAGATGATGATGATGATGATGATG
 ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAAGCCATTCTCCA
 TTTGATCTGTTCCAATGTGTCCATTGGATGTCAGTGCTATTACAGAGTTGATCTGCTC
 AGATTTAGGTTGACCTCAGTCCAACAAACATTGATACTCGAATGCTTGATCTC
 AAAACAATAAAATTAGGAAATCAAAGAAAATGATTTAAAGGACTCACTCACTTATGGT
 CTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTCTAACCAAAAGAA
 GTTGCAGGCTGTATCTGCCCACAATCAACTAACAGTGAATACCACTTAATCTCCCAAAT
 CATTAGCAGAACTCAGAATTGAAAATAAGTTAAGAAAATACAAAGGACACATTCAA
 GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTATAATGGGATAGA
 GCCAGGGGATTGAAGGGGTGACGGTGTCCATATCAGAATTGAGCAGAAACTGACCT
 CAGTCCTAAAGGCTTACCAACATTATTGGAGCTCACCTAGATTATAAAATTCA
 ACAGTGGAACTTGAGGATTTAAACGATACAAAGAACTACAAAGGCTGGCCTAGGAAACAA
 CAAAATCACAGATATGAAAATGGAGTCTGCTAACATACCACGTGAGAGAAATACATT
 TGGAAAACAATAAACTAAAAAAATCCCTTCAGGATTACCAAGAGTTGAAATACCTCCAGATA
 ATCTCCTTCATTCTAATTCAATTGCAAGAGTGAGTAAATGACTTCTGTCCAACAGTGCC
 AAAGATGAAGAAATCTTATACAGTGAATAAGTTATTCAACAAACCCGGTGAATACTGGG
 AAATGCAACCTGCAACATTGTTGTTGAGCAGAATGAGTGTCACTGGAAACTTT
 GGAATG**TA**ATTAGTAATTGTAATGTCCATTAAATATAAGATTCAAAATCCCTACATT
 TGGAAACTTGAACTCTATTAAATGGTAGTATTATATAACAGCAAATATCTATTCTCA
 AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAATTGCAAACACTATT
 GATACATAAGGGGTTGAGAGAAACAGCATCTATTGAGTTCCCTTGTACAAATGAT
 CTTACATAATCTCATGCTTGACCATTCCTTCTTCATAACAAAAAGTAAGATATTGCGTA
 TTTAACACTTGTATCAAGCACATTAAAAGAACTGTACTGAAATGGAATGCTTGACT
 TAGCAAAATTGCTCTTCATTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT
 GAAGAGTGCATTACACTATTCTTATTCTTAGTAACGGTAGTACTGAAATATTAAAT
 CATCTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATGCTTAGAGCCGT
 CTTATGTTAAAACATAATTCTAAAATAAGCCTCAGTAAATGTTATTACCAACTGTA
 TAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTAATTATT
 ACCTGATTAAAATCTGTAAAAACGTGAGTGTTCATAAAATCTGTAACCGCATT
 AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
 TTCAACTCTAAGGAATATTGAGATATCCCTTGGAGACCTTGCTTGGAGAGGCCTGGA
 CACTAACATTACACCAATTGCTCTTCATAACGTATGGACTGGATAACTCTGAGAAA
 CACATCTAGTATAACTGAATAAGCAGAGCATAACAAACAGACAGAACCGAAAGCTCTA
 TATAATGCTAGAGTTCTTATGTTATTGTCATTGAGCATTCAACATATGAAAATCAGAAA
 ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

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DRAFTSMAN	CLASS SUBCLASS

FIGURE 2

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, PI: 7.30, NX(S/T): 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDSLFPTRREPR
SHFFPFDFLFPMPGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL
KYLQIIIFLHSNSIARGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
```

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 3

CGGACGCGTGGCGGACGCGTGGGCCGSGCACCGCCCCGGCCCTCCGCCCTCCGACTCGGCCCTCC
 CTCCCTCCGCCGCTCCCGCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC
 GGCCCCGCCGGCCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGCCGCCAGA
 GCCCCCCGTGCTGCCATCCGTCTGAGAAGGAGCCGCTGCCCTGGGAGCGGCAGGCTGACCTTCGGCG
 GAAGGTCTATGCCTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTGGGGTGTGCGCTGCGTGTG
 CGCCTGCGAGGCGCCTCAGTGGGTGCGCGTACCGGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACAGA
 GTGCCCAACCCGGCCTGTGGCAGCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCAGGAGCGCAG
 CAGTCGGAGCGGAGCCGAGCGGCCGCTGCTCCCTCGAGTATCCGCCGGGACCCGGAGCATCGCAGTTATAGGACCG
 CGGGGAGCCAGGCGCTGAGGAGCGGGCCCGTGGTACGGCCACACGGACTTCGTGGCGCTGTCAGCAGGGCCGAG
 GTCGCAGGGGGTGGCACGAGCCGAGTCTGCTGCTAGCCTCCGTTCTATCTCTACAGGGGGCT
 GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCTGCAAGCCCCACCCA
 AGATGGCCTGGTCTGTTGGGTGAGGAGCCGACTGCCCTGGTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
 TGTGGCACTTGTGACACTCACTCACCTTCAGGGAGGTCTGGGGCCTCTCATCCGGCACCGGGCCCTGGCTGC
 AGAGACCTTCAGTGCATCCTGACTCTAGAACGGCCCCACAGCAGGGCGTAGGGGCATCACCTGCTCACTCT
 CAGTGACACAGAGGACTCCCTGCAATTTCGCTGCTCTCCGAGGGCTGCTGGAACCCAGGAGTGGGGACTAAC
 CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACCTCAGGCAATGTCTCAGCCCA
 GGAACCAGGCTTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGACTGGCTGGTCTGGGGAGCTGCA
 GATGGCCCTGGAGTGGCAGGCAGGGCTGCGCATAGTGACACATTGCTGCCAGGAAGAGCTGGACGT
 CCTGCAAAGTGTCTTGTGGGCTGATGCCCTGATCCCAGTCCAGACGGGTGCTGCCGGCTAGCCAGCCTCAC
 GCTGCTAGAAATGGCTCCCTGATCTATCAGGTGCAAGTGTAGGGACAAGCAGTGAAGGTGGTGGCCATGACACT
 GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCCTGTGCCACATGGCTGGACTCCAGCAGGAGGACACAC
 GGCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGCTATATGCTGTCAGAATGAGCTTCTGAACGT
 GGGCACCAAGGACTTCCCAGACGGAGAGCTCGGGCACGTGGCTGCCCTACTGTGGCATAGGCCCG
 CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
 CTGGCTTCCCTGGATACCCACTGTCACCTGCACTATGAAGTGTGCTGGCTGGCTGGCTCAGAACAAAGG
 CACTGTCACTGCCACCTCCTGGGCTCTGGGAACGCCAGGGCCTCGGGCTGCTGAAGGGATTCTATGGCTC
 AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGAATGCTGGCACCTGGCAAAAGGCATGGCTCCCTGAT
 GATCACCACCAAGGGTAGCCCCAGAGGGAGCTCGAGGGCAGGTGCACTAGCCAACCAATGTGAGGTTGGCGG
 ACTGCGCTGGAGGCCGGCCGGGGCGAGGGGTGCGGGCGTGGGGCTCCGGATACAGCCTCTGCTGCCGCC
 TGTGGTGCCTGGTCTCCGCCCTAGGCCCGCAAACCTGGTGGTCTGGGCCGGGGCGAGAACCCAAACATG
 CTTCTCGAGGGCAGCGGCCACCGGGCTCGCTGGGCCCAAACACTACGACCGCTCTGCTCACTCTGAC
 CTGCCAGAGACGAACGGTATGTGACCCGGTGGTGTGCCACCGCCAGCTGCCACACCCGGTGCAGGCTCC
 CGACCAAGTGTGCCCTGTTGCCCTGAGAAACAAGATGTCAGAGACTTGCCAGGGCTGCCAGGAGCCGGACCC
 AGGAGAGGGCTGCTATTGTGATGGTACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCGGTGTGCC
 CTTGGCTTAATTAAGTGTGCTGTGCAACCTGCAAGGGGGACTGGAGAGGTGCACTGTGAGAACGGTGCAGTG
 TCCCCGGCTGGCTGTGCCAGCCGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGGCTGG
 GGCCACCCAGCTGGGGACCCCATGCAAGGCTGATGGGCCGGGGCTGCCGTTTGCTGGCAGTGGTCT
 AGAGAGTCAGAGCTGGCACCCCTAGTGGCCCTTTGGAGAGATGAGCTGTATCACCTGCAAGATGTGGGAG
 GGTGCTCACTGTGAGCGGGATGACTGTTCACTGCACTGTCCTGTGGCTGGGGAGAGAGTCAGTGTGTT
 CCGCTGCAAGGCCACCGGGCCCCAGAGACCAAGCAGACTGATCCAGAGCTGGAGAGAACGCCAGGAGCTT
 GGGAGCAGCCAGAGGGCAAGTGAACCAAGAGGATGGGCCCTGAGCTGGGAAGGGGTGGCATCGAGGACCTT
 GCATTCTCTGTGGGAAGGCCAGTGCCTTGCTCCTCTGTGCCCTACTCCCACCCACTACCTCTGGGAA
 CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTGACAGCCACTCCAAGTCTGCCACCC
 TCGGCTCTGTCTGGAAAGCCCACCCCTTCTCTGTACATAATGTCAGTGGCTTGGGATTTTAATT
 TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATGGAGAG
 TTTGTATTTATTAAAACATTCTTTTCAGTCAAAAAAAAAAAAAAA

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FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRAAGCTFGGKVYALDE
 TWHPDLGQPFGVVMRCVLCACEAPQWGRTRGPGRVSKNIKPECPTPACGQPRQLPGHCCQT
 CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDGHTDFVALLTGPRSQAVER
 ARVSLLRSSLRFSISYRRLLDRPTRIRFSDNSGSVLFEPAAPTQDGLVCGVWRAPRLSLRL
 LRAEQLHVALVTLTHPSGEVGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED
 SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPEGFAEVLPNLTVQEMD
 WLVLGELQMALEWAGRPGRLRISHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
 GSЛИYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
 LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPPVKSQAAGHAWLS
 LDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTPGPRRLLKGFYGSSEAQGVVKDLEPELLR
 HLAKGMASLMITTGSQPRGELRGQVHIANQCEVGGLRLEAAGAEGRALGAPDTASAAPPVV
 PGLPALAPAKPGGPRPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRRTVICDPVVCP
 PPSCPHPVQAPDQCCPVCPEKQDVRLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPPF
 GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCCKQCPVGSGAHPQLGDPMQADG
 PRGCRFAGQWFPEQSWSHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS
 RCTAHRRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
 390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
 576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
 905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

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FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTGCCTGCCACTGCCACCGCCGCCGCGTCACTGCG
TCCCTGGCTCCGGCTCCCGGCCCTCCCCGGCCGGCCATTCGAGCCCCGCCGCCAGGCGCCGGTGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTCGAGCGGGGCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG
CCCGGCCCTTGTCTGCGCCCCGGCCGTGCAGCCGAGCCCTGCCGAATGGGGTGTGTCACCTCGGCCCTG
AGCCGGACCGCAGCACCCGGCCCCCGCCGGAGGCCTGGCTACAGCTGCACCTGCCCGGCCGATCTCCGGCG
CCAACCTGCACTGTTGCACTCCTGCAACCCCTGTCACCATGGCAACTGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCAATTGCAATGAAGGCTATGAAGGTCCTAACACTGTGAACAGGCACTTCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCCTGTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCTCGCTCTCAGGCAACGGTACACTGCCTACCTGGCAGCGAAAACAGGGCAGAAAGTTGTAGAAA
TGAAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC
GCCTGGTATCCTTGAAGTGCCACAGAACACCTCAGTCAGTCAGATTGCCAAGATGCCACTGCCACTGATTG
TCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACAGTGTGACCCCCCTCAGGCTT
CAGGGGGACTGGCTCTGGAGGAGATGCTGCCCTGGGAATAATCACTTATTGGTTTGTGAATGATTCTG
TGACTAAGTCTATTGTTGGCTTGCCTAACCTGGTGGTAAGGTCAGCACCTGTGTGCCGGGGAGAGTCAGC
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCAGAACAGCCGTAGAGGCAACTTTCTGACCTGTG
AGGAGCAGTACGTGGGTACTTCTGTAAGAATACGATGCTGCCAGAGGAAACCTTGCACAAACACGCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTGCCCTGGTTACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCTAGACCATGCAAGAACATGCATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTCGGATCTGCTGTGAAGAAAAGGTGGACCCCTGCCCTCGCTCTCCGT
GCCAGAACACGGCACCTGCTATGTGACGGGTACACTTACCTGCAACTGCAGCCGGCTTCACAGGGCCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGGCCACCAGCT
ACAAATGCCCTGTGATCCAGTTACCATGCCCTACTGTGAGGAGGAATATAATGAGTGCCTCTCGCTCCAT
GCCCTGAATGCAGCCACCTGCAAGGGACTCGTTAATGGCTATGAGTGTGTGCCCTGGCAGAAATACAAGGAACAC
ACTGTGAATTGACAAGGATCCCTGCGCTAACGTCAGCTGTGCAACGGAGCCACCTGTGACAGCAGGCCGTGA
ATGGCACGTGCATCTGTGCAACCGGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGAGCTGCCCTGCCAGGCCAATGGTTATAACTGCCACTGCCGCATGGTTGGGTGGAG
CAAACGTGAGATCCACCTCCAATGGAAGTCCGGCACATGGCGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATGGAGGCCCTCGCTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGATTGCCGCA
TCAGCCGATTGAATACCAGGGTTCTCCAGGCCAGCTATGAGGAGTTCTACAAACTGCCAGCATGACAGCG
AGTTCAGCAATGCCATTGCACTCCATCGGCATGCCAGGTTGGAAAGAAATCCGGCCTGCAATGTATGATGTGA
GCCCATGCCATGAAGATTACAGTCTGATGACAAACCTGGTCACACTGATTAAACTAAAGATTGTAAT
CTTTTTTGATTATTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTAAGAAAATAAAAGCTTAA
GAAATTAAAATGCTAGCTCAAGAGTTTCAGTAGAATATTAAAGAACTAATTTCTGAGCTTTAGTTG
AAAAAAATTTAAAACAAAATTGTGAAACCTATAGACGATGTTTAATGTACCTCAGCTCTAAACTGT
GTGCTCTACTAGTGTGTGCTCTTCACTGTAGACACTATCACGAGACCCAGATTAAATTCTGTGGTTGTTACA
GAATAAGTCAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCAGGCCGTTCTGAGTAGAGTTAGGAAAACAC
GTAACGTAGCATATGATGTATAATAGAGTATACCGTTACTAAAAAGAAGTCTGAAATGTTGTTGTGAAAC
AGAAAATAGTTAAATTACTATTCCCTAACCGGAATGAAATTAGCCTTGCCTTATTCTGTCATGGGTAAGTAAC
TTATTCTGCACTGTTGTAACCTTGAGGAAACATTCTTCAGGTTGTTGTCATTCTGTAACAGTCG
TCGAACTAGGCCCTCAAAAACATACGTAACGAAAAGGCCAGCGAGGCAAATTCTGATTGATTGAAATCTATATT
TTCTTTAAAAGTCAGGGTTCTATATTGTGAGTAAATTAAATTACATTGAGTTGTTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTCCTCAGTAGTGTAGTATTCTCATAGTGCAGCTTATTATCTCCAGGATGTT
TTTGTGGCTGTATTGATTGATATGTGCTCTCTGATTCTGCTAATTCCAACCATATTGAATAATGTGATC
AAAGTCA

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FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALLLLLLGAGPRGSSLANPVAAPLSAPGPCAAQPCRNGGVCTSR
 PEPDPQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN
 EGYEGPNCEQALPSLPATGWTESMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV
 VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
 QCSLIDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTVVKVSTCVPG
 ESHANDLECSKGKCTTKPSEATFSCTCEEQYVGTFCCEYDACQRKPCQNNASCIDANEKQD
 GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
 ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG
 YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAELYKGTACHELYKDPCANVSLNGATC
 DSDGLNGTCICAPGFTGECDIDINECDSNPCHGGSCLDQPNNGYNCHCPHWVGANCEIHL
 QWKSGHMAESLTNMPRHSLYIIIGALCVAFILEMLIILIVGICRISRIEYQGSSRPAYEEFYN
 CRSIDSEFSNIAISIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
 375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
 373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
 491-503, 529-541, 567-579, 605-617

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FIGURE 7

CTCTGGAAGGTACGGCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTAAGGTAGCACCTGTGCCCCGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

TOP SECRET - SECTION 1

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FIGURE 8

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTTCAAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGAG

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FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
 GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
 GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT
 GATGCGGGACTTCCCCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT
 ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGCCAGACCAGCCTGGAC
 AGGCTTAGAGATGCCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
 GGACCGGGATGCCCTCGCCTCACCCCTGGAGCAGATTGACCTCATGCCGATGTGTGCCT
 CCTATTCTGAGCTGGAGCTTGACCTCGCTAAAGCTCTGAACGACACTCAGAAATTGCC
 TGCCTCATCGGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
 CTACATGCTGGAGTGCCTACCTCCTCTACAACAAACATCAGGGCTGACTGACTTTGGTGAG
 GCTCCGCTAAGGGGTCCACTCCTCTACAACAAACATCAGGGCTGACTGACTTTGGTGAG
 AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
 TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCCTCGCTGCC
 GGGGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAGAAC
 GGTGGCGTCGTGATGGTGTCTTGTCCATGGAGTAATACAGTGCAACCCATCAGCCAATGT
 GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGA
 TTGGTGGAGATTATGATGGGCCGGCAAATTCCCTCAGGGCTGGAAGACGTGTCCACATAC
 CCGGTCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCT
 TCGTGGAAACCTGCTGGGTCTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
 AAAGCCCCTGGAGGACAAGTCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC
 TCACGTCTGCGTCAGAGACAGAGCTGACTTCAGGCCAGGAACACTGAGATTCCCATA
 CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
 TCCTTGCAGTTGTGGCACCTTCCAGTCCTATTCTGTGGCTTGATGACCCAGTTAGTCC
 TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
 AATATTCCCTGAAATAATGTTGGACATAG

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FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pi: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAE MNRLGMMVDLSHVSDAVARALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQS PLEDKFPDEQLSSS
CHSDL SRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 11

AAAACCTATAAATATTCCGGATTATTACATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
 CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
 CCCAGGGCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCCTCGTGGACGGCCAC
 AACGACCTGCCCTGGCTTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
 CAATTCAGCTACGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT
 TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
 CAGATTGACCTCATGCCGATGTGTGCCCTATTCTGAGCTGGAGCTTGACCTCGC
 TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCATCGGTGTAGAGGGTGGCCACTCGC
 TGGACAATAGCCTCTCCATCTTACGTACCTCTACATGCTGGAGTGCCTACCTGACGCTC
 ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAACGGCGTCCACTCCTTCTACAA
 CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGCAGAAATGAACCGCCTGGCA
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
 GCACCTGTGATCTTCTCCACTCGGCTGCCGGGGGTGTGTGCAACAGTGCTCGGAATGTTCC
 TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCCATGG
 GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
 AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
 CCCTCAGGGGCTGGAAGACGTGTCACATACCGGCTCTGATAGAGGAGTTGCTGAGTCGTG
 GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGGCTTCAGACAA
 GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAAGTTCCCGATGA
 GCAGCTGAGCAGTCTGCCACTCCGACCTCTCAGTCTCGTCAGAGACAGAGTCTGACTT
 CAGGCCAGGAACACTGAGATTCCCATACTGGACAGCCAAGTTACAGCCAAGTGGTCA
 GTCTCAGAGTCCTCCCCCACCCTGACAAAACACATGCCACCGTGCCAGCACCTGA
 ACTCCTGGGGGACCGTCAGTCTCCTCTCCCCAAAACCCAAGGACACC

DRAFTED - 03/09/2018

APPROVED	U.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLA CLIGVEGGHSLDNSLSILRTFYMLGVRYLTLCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNR LGMMV DLSHVSDA VARRA LEVS QAPVIFSHSA ARGVCNSARNVPDDILQ
LLKKNGG VVMVSL SMGVIC QCNPSANV STVADHFDHI KAVIGSKF I GIGGDYDGAGKF PQGLE
DVSTYPV LIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEE KWQS PLEDKFPDEQLSSS
CHSDL SRLR QRS LTSGQ ELTEIPIHWTAKLPAKWSVSESSPHDKTHTC PPPCPAPEELLGGP
SVFLFPPPKPKDT

TOP SECRET - EYES ONLY

APPROVED BY	O.G. FIG. CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 13

CGCCCAGCAGCTGCGGGCGGCCCTGGCCCGCCCTCCCGCGCCCGCTCGTCCCCGCGCC
CTGCGCACCGCCGCCAGCCAGCCCCGCCGCCAATCCGCGGGCGGCCGCGCCGTTGCTGCCCTGCT
GCCGGCCGCCGGGCCCCGCCGCCAATCCGCGGGCGGCCGCGCCGTTGCTGCCCTGCT
GCTGCTGCTCTCGTCCTCGGGCGCCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCAGGGCCTCTACTGGACCCCTAACGGCGCCGCTGCC
TGAGCTCTCCCGTGTACTCAACGCCTCACCTGGCTCTGGCCCTGGCCAACCTCAATGGGT
CCAGGGCAGCGGTGGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGGC
TCCTGCCTCTATGTTGGCCTGCCCTGCCCCAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCTCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGCACGTGAGCCGCTGGGGGCTGGAG
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTCAAGGATTCCTCTTCAAGCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCGGCCCTGAAACCCGGCACCGTGTACTTCGTCAAGTGC
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTCCACTCCCCGAGCTGAGCGCCGGCCGGCGAGCTCAAGCAGTTCTGGCTGGCTC
GGGGCGAGAGCCGAGCTGGGGCGGTGCGCGAGCTCAAGCAGTTCTGGCTGGCTGG
AAGAAGCACCGTACTGCTCCAACCTCAGCTTCCGCCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA
CGGCGAGAGGTCTGCCAGATAAGCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA
CGCAGAGGCCAACCAAACGGGCCACCTCTGTACCCCTACTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCAACGCCATAACAGCTCTGACTCCACGT
GAGGCCACCTTGGGTGCAACCCAGTGGGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTAAATAAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

APPROVED BY	O. G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLGVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNRRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRGSAVDVLTLIDILDVVTTDPPPDVHSVSRVGG
LEDQLSVRVWSPPALKDFLFQAKYQIRYRVEDSDWKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRRGRTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

APPROVED BY	O. G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
 AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
 CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
 GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTGCTAAACTTAAAGCAAGCTGGTTCTCTGGATATAAATAAG
 CATGGACTGGAGAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTTACACCTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
 CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA
 GGCATTCTCCTGCAATGACGAAGAATAACCATGCCATTGTCAGTGGCTTCGGCAG
 CTGGACATGTCTGGTCCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA
 TTTCATAAAACTTGACAGATGAACGGCTGCCTTACAAATACTGGAGTCAAAACACATG
 TCTGTGTCCTAATTCGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
 ATTTTATTCCATCTTCTATAGCTTTTAACAAACATTGAAAGGATCCTGAGCGTT
 CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTGAGTAAAGTAA
 AAGCGCAATAGCACCTAGTTCTGAAAACGATTTACCAAGGTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTTCAATA
 TCATTGGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAGAA
 CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
 AATTGTACCAACCGTTATTAAACATATATTATTGATTGACTAAATTGTT
 ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA
 TGAAGGACTATCTAGGGTATTTCACAATGAATATCATGAACCTCAATGGTAGGTTTC
 ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAAACATTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAA

SEARCHED - INDEXED - SERIALIZED - FILED

APPROVED BY	O G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, PI: 9.52, NX(S/T): 1
MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHSVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

TOP SECRET//NOFORN

APPROVED BY DRAFTSMAN	O G. FIG. CLASS SUBCLASS
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FIGURE 17

G 9514369 D 89 004

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GACTAGTTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCAAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATGGGGAGCCGGAGGGGGACT
GCGAGAGGACCCCGCGTCCGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
TGCTCCTGGCCTGGCGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGACCCCGGCCTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTGCCGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCCGGCTCCGGGAGAGAAAGGCAGGGGGAGGGGG
GGCCGGGACTGCCGGGACCTCGAGGGGACCCGGGCCGCGAGGAGAGGCAGGGACCCGGGG
CCCACCGGGCTGCCGGGAGTGCTCGGTGCCTCCCGATCCGCCTTCAGGCCAACCGCTC
CGAGAGCCGGGTGCCTCCGCGTCTGACGCACCCCTGCCCTCGACCGCGTGCCTGGTAACG
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCCTGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTAAGAAATGGCGA
ATCCATTGCCCTTTCCAGTTTCGGGGGGTGGCCAAGGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTGCTTAGGCCACTGCAAAGTGAGCTATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTACCCAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGATTTCTGCCCAAGACCA
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGCAGTGGCTGGATTTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGTGCTCTTCCCTGGCTCTGCTTCTGGATCCTCCCCACCCCTGCTGCTCTGGG
GCCGCCCTTCTCAGAGATCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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APPROVED BY	O.G. FIG.	
DRAFTSMAN	CLASS	SUBCLASS

FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
><MW: 25298, pI: 6.44, NX(S/T): 0
MRPLLVLLLLGLAAGSPPPLDDNKPSSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRGPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKT DSTFSGFLVYSDWHSSPVFA
```

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

APPROVED BY	O. G. FIG. CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
 AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGACACCTGACGGGCCAACAGACCC**AT**
GCTGCATCCAGAGACCTCCCCTGGCGGGGCATCTCCTGGCTGTGCCTGGCCCTCCTG
 GCACCACCTGGCAGAGGTGTGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCGGAGCC
 CTGAACAGGAAGGAGAGTTCTTGCTCCTCTCCCTGCACAACCGCTGCGCAGCTGGTCCA
 GCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG
 CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCTG
 CAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTGTGAAGTGGTCAG
 CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCGCAGGAGAGTGTGCTCGCAACGCCA
 CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC
 CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCTTGTCTGCTACTCCCCGGAGGCAA
 CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTGCTCTGCA
 CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCC
 AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG
 CCACTGTCCCCCTGGCTACACGGGAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
 ACGGCCGGTCCGGAGGAGGTGCTCGTGTGACATCGGCTACGGGGAGGCCAG
 TGTGCCACCAAGGTGCATTTCCCTCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
 CATGGTGTCTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
 GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGAGGACATCCTCGCCTTCTATCTGGCCGC
 CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGGCT
 CACCTACAAGACGCCAAGGACTCCTCCGCTGGCCACAGGGAGCACCGCCCTCACCA
 GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT
 GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTCAACTGGAACGACCAGCGCTGAAAAC
 CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGGCCAGGGCCT
CG**AGGCCTGACCACATGGCTCCCTGCCTGCCCTGGAGCACCGGCTCTGCTTACCTGTCTGC**
 CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
 CCTTGACAATGCCAGAAGTTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
 AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTTGATTGGAAAGATGGGCTTCAATTAGA
 TGGCGAAGGAGAGGACACCGCCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCAGAC
 CCTGTGGGGCAGCGGAGCTCCCTGTGGCATGAACCCCACGGGTATTAAATTATGAATCAG
 CTGAAAAAAAAAAAAA

APPROVED BY	O. G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pi: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQA
PMAGALNRKESFLLLRLHNRLRSWV
QPPAADMRRLDWSDSLQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLWATSSQLGCGRHLC
SAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWSLCTASVSGCFKA
WDHAGGLCEVPRNPCRMS
CQNHGRLNISTCH
CHC
CPPGYTGRYCVRC
SLQCVHGRF
REEEC
SCVCDIGYGG
AQCATKVHF
FPFHTCDLR
IDGDC
FMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEV
TDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAF
TSFAFGQPD
NHGLVWL
SAAMFGNC
VELQASAA
FNWNDQRCK
TRNRYICQFA
QEHI
SRWGP
GS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

APPROVED BY	O. G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 21

CGGACGCCTGGGCTGGCGCTGCAAAGCGTGTCCGCCGGTCCCCGAGCGTCCCCGCCCT
CGCCCCGCCATGCTCCTGCTGCTGGGCTGTGCCCTGGCTGTGAGCTCAGGCTCCGAGGAAG
GGAAGAGGCGCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGCTCCGAGGAAG
TCAGACTGTTGCAGAGGCTGAAAACAAACCTTGTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCCTTATGCCTTCACTACGGTTCTGCAGAATGCTGAACAGAGCTCTGAAGA
CCAGGACATTGAGTCCAGATGCAGATTCCAGCTGCAGCTTCACTACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGTAGG
GTAAAAGAGAAAAGGAATAAACACAGAAGAAAATGGAGAGAAGGGACTGAAATATTCAAG
AGCTTCTGCAGTGATTCCCAGCAAGGACAAGGCCCTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCTGGCAAGTACGAGCACAGCATCAGCGTGCAGCCCCAGCAGCTGCC
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACACAGCAGGCAGAGGGGCAGTGGCGCGGGAAAGATGATTCTGGCCTCCCCAT
CTACTGTCATTAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAATGAAATTGGAGACTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTGTGCACTACTTGCTCCTA
AAGACCTTCCTCCTTACCCAAGAATGTGGTATTGCTGACAGCAGTGCCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTTCAACATTCTCATGACCTCCGACCCCA
GGACCGTTCACTATGGATTTCACGGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTCAACATATGTCACCCACTGGA
GGCACAGACATCAACGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAGTACGTGGCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATGCTTCTGACGGATGGGAAGGCCACGG
TCGGGGAGACGCACACCTCAAGATCCTCAACAAACACCCGAGAGGCCCGAGGCCAAGTC
TGCATCTTCACTATTGGCATGGCACAGCAGTGGACTTCAGGCTGAGAAACTGTCGCT
GGAGAACTGTGGCCTCACACGGCGGTGACGAGGAGGAGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCGCTCCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCAACTACTTCACGGCTGGAGATCATCAT
TGCGGGGAGCTGGTGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCCTGGAGGCCATGGAGAGGGGACACCAACCACATGAGCGTCT
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGAACGATGAACCGG
AGAAGGAGCGCTGCCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCACTCCC
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACGCATGGATGCCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGGACCCGAACGGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAAAACAAACAAAAACAAAAAAGA
CATGGGAGAGATGGTGTGTTCTCCTCCACACCTGGGATACGATGAGAAGATGCCACCT
GCAAGCCAGGAAGACGCCCTCACAGACACCATGTCTGCTGGCACCTGATCTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pI: 9.54, NX(S/T): 6
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE
KRNKTTEENGEKGTEIFRASAVIPSVDKAFFLSYEELLQRRLGKYEHSISVRPQQLSGRSL
VDVNILESAGIASLEVPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHЛИSVPDСIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 23

DRAFTS: 6-08300

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCAGCGGATCCCAGTGTGC
 GGCAGCGCGCGCGCGCCTCCGGCTCCGGCTTGCTGCTCTTCTCCGCCCG
 CACTGATCCCCACAGGTGATGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGG
 GAGGTTGCGACCATCAGTGCAAGTCATAAGAGTGACGACTCTGTGATTCA
 TCCCACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGACAGCAGGTT
 TGCTGAATTTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA
 GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
 CCTGGTCCCACCGTAATCTGATGATCGATATCCAGAAAGACACTCGGGTGAAGGTGAGG
 AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCCACGACTATCAGGTGGTT
 GGGAACACAGAGCTAAAGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
 CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACATGGGTCCCAGTGATGCCAGGTGG
 AGCACCCCTGCCGTCACTGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
 CAAGTGCACATTGAGTACTTACCTCTACAAGGCTTAACCCGGAAAGGGACGCGCTTGA
 GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACGGTGGTGAAGAGTC
 ATGAAATGCCAACACGCCGTACTGTCTGGGCCAACCTGTTACATAAACCTAAACAAA
 ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGAAAGCTCACTCGGATTA
 TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCTCCCACAACAACCACCA
 CCACCAACCACCAACCACCATCCTACCATCACAGATTCCGAGCAGGTGAAGAAGGC
 TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGGCGGTGGTGGTGGTGC
 GCTGTGCTTGCTCATCATTCTGGGGCGCTATTGCCCCAGACATAAGGTACATA
 ATGAAGCCAAGGAGCCATGACGCAGCAGACACAGCTATAATCAATGCAGAAGGA
 GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTGTTCAAT
 GAGGTGTCCAACGGCCCTATTAGATGATAAGAGACAGTGATATTGG

APPROVED BY	O G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pi: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIVFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTNGTYR
CEASNIVGKAHSDYMLYYDPPTTIPPPTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

APPROVED BY	O. G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 25

GGGGCGGGTGGACCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGA
 CCCGCCAGGAAAGACTGAGGCCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTA**C**TGGCCCT
 GGGGCTGGGTGCAGGGTGCCTGCCCATCCGGCTGCCAGTGCCAGGCCACAGACAGTCTTCT
 GCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC
 GTCTTGAGAACGGCATCACCATGCTGACGAAGCAGCTTGCCGGCTGCCGGGCTGCA
 GCTCCTGGACCTGTCACAGAACAGATGCCAGCCTGCGCCTGCCCGCTGCTGCTGG
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCATCCTGGACACTGCCAACGTGGAG
 GCGCTCGGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGGCTTCAGCCGCTGCG
 CAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGCCTGACGCCCTGCCGGCAACACCCGATTGCCAGCTGCCGG
 GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGC
 CCTGCCCTGGCACCTCTGGGCCTTCCCCGCCCTGCCGGCTGCTGGCAGCTGCCGCAACC
 CCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACA
 CTGGCCAGCCCTGAGGAGACGCCCTGCCACTTCCGCCAACAGCCTGGCCGGCTGCTCCT
 GGAGCTTGA~~T~~ACGCCGACTTGGCTGCCAGCCACCACAGCCACAGTGCCAACCA
 CGAGGCCGTGGTGCAGGGAGCCACAGCCTGTCTAGCTTGGCTCCTACCTGGCTTAGC
 CCCACAGGCCGGCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCC
 TGTCCCCAGCCCCAGGACTGCCAACCGTCCACCTGCCCAATGGGGCACATGCCACCTGG
 GGACACGGCACCCACTGGCGTCTGTGCCCGAAGGCTTACGGGCTGTACTGTGAGAGC
 CAGATGGGGCAGGGACACGCCAGGCCACACCAGTCAGGCCAGGGCCACCACGGTCCCT
 GACCCCTGGGATCGAGCCGGTGA~~G~~CCCCACCTCCCTGCCGTGGGCTGCAGCGCTACCTCC
 AGGGGAGCTCGTGCAGCTCAGGAGCCTCCGTCTCACCTATGCAACCTATGGGCCCTGAT
 AAGCGGCTGGTGA~~G~~CTGCCACTGCCCTGTGTCATGCCCTTGGGCCGGGCGGGTGCCGGAGGGCG
 GCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGGCCGGGCGGGTGCCGGAGGGCG
 AGGAGGCCGTGCCGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCAGTCACC
 CAGGCCCGCAGGGCAACCTGCCCTCCTCATGCCGCCCTGGCGGGTGTCTCTGGC
 CGCGCTGGCTGCCGTGGGCTGGGCCAGCCTACTGTGTGCCGTGGCGGGGCCATGGCAGCAGCG
 CTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGA~~A~~CTGGAGGGAGTGAAGGTC
 CCCTTGGAGCCAGGCCAGGCCAACAGAGGGCAGGTGGAGAGGCCCTGCCAGCGGGTCTGA
 GTGTGAGGTGCCACTCATGGCTTCCAGGCCCTGCCCTCCAGTCACCCCTCCAGCAAAGC
 CCTACAT**TAA**GGCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC
 CAGGCCCTCCCTGCCAACGTCAAGTCTCAGTCCAAACCTCGGGATGTGTCAGA
 CAGGGCTGTGACCACAGCTGGCCCTGTTCCCTCTGGACCTCGGTCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT
 CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAGGGCAGGGCCCTGCCATGTGCTGTAAC
 GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGCCAGGCCCTGGGGCCAGTGAAGGAAG
 CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTCTAGTCTTGGCCAGG
 AAGCGAAGGAACAAAAGAAACTGGAAGGAAGATGCTTAGGAACATGTTTGCTTTTAA
 AATATATATATTTATAAGAGATCCTTCCATTATTCTGGGAAGATGTTTTCAAACTC
 AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATATGAAGGCCTTGTAAAGAAAAAA
 ATAAAAAAAAAA

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APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pi: 7.24, NX(S/T): 3

MCSRVPLLPPLLLLALGPGVQGCPGQCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
 GITMLDASSFAGLPGQLLQLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDNTANVEALRL
 AGLGLQQQLDEGLFSRLRNLDLSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
 GLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPNCVCPLSWFGPWVRESHVTLASP
 EETRCHFPPKNAGRLLELDYADFGCPATTTATVPTTRPVVREPTALSSLAPTWLSPTAP
 ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLA CLCPEGFTGLYCESQMGQ
 GTRPSPTPVTPRPPRSLTGLIEPVSPSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV
 TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPAVHSNHAPVTQARE
 GNLPPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQVGPAGPLELEGVKVPLEP
 GPKATEGGEALPSGSECEVPLMGPGLQSPHLAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

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APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 27

GGCACTAGGACAACCTTCTCCCTCTGCACCACTGCCGTACCCCTACCCGCCCGCACC
 TCCTTGCTACCCACTCTGAAACCACAGCTGGCAGGGTCCCCAGCTC**ATGCC**CAGCCTC
 ATCTCCTTCTTGCTAGCCCCAAAGGGCTCCAGGAAACATGGGGGCCAGTCAGAGAGC
 CGGCACACTCAGTTGCCCTGGTTGAGTTGGGGCAGCTCTGGGGCGTGGCTTGCC
 ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
 GGGGACAGGAGGCCCTCCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA
 GTTCCGATGCCCTGGAAGCCTGGAGAAATGGGAGAGATCCGGAAAAGGAGAGCAGTGCTC
 ACCCAAAACAGAACAGAACAGCAGCACTCTGTCCTGCACCTGGTCCATTACGCCACCTCAA
 GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTAGGCGTGGAGAGGCCTAC
 AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTATGCCAGGTC
 CTGTTCAAGACGTGACTTCAACCATGGTCAGGTGGTGTCTCGAGAACGGCAAGGAAGGCA
 GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACGGGCCTACAACAGCT
 GCTATAGCGCAGGTGTCTCCATTACACCAAGGGATATTCTGAGTGTCTAAATTCCCCGG
 GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACT**TGATT**
 GTGTTATAAAAGTGGCTCCCAGCTTGGAAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
 GAGCTGAGTATATAAGGAGAGGAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC
 CCCGTTCTCACTTTCCCTTTCATCCTCCACCCCTAGACTTGATTTACGGATATCTTG
 CTTCTGTTCCCCATGGAGCTCG

P-051136-100380-1

APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, PI: 9.85, NX(S/T): 2

MPASSPFL LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQN GEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSQLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR IQDAGVYLLYSQVLFQDVFTMGQVVSREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVI I PRARAKLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

APPROVED	O. G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

FIGURE 29

CACTTCTCCCTCTTCCTTACTTCGAGAAACCGCGCTCCGCTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGTGGGGGACCTGTGGCTGCTCGTA
 CCGCCCCCCCACCCCTCCTCTGCACTGCCGTCCCGAAGACCTTTCCCCTGCTCTGTT
 TCCTTCACCGAGTCTGTGCATGCCCGGACCTGGCCGGAGGAGGCTGGCCGGGGAGA
 TGCTCTAGGGCGGCCGGAGGAGCAGGCCGGAGGAGGGCCCGCAGGAAGATGGGC
 TCCCCTGGACAGGGACTCTGCTGGCTACTGCCTGCTCCTGCCTTGCGCTCTGGCCTGGT
 CCTGAGTCGTGTGCCCATGTCAGGAGTGGAGGGACTGAGGAGCTGC
 CGTCGCCTCCGGACCATGCCAGAGGGCTGAAGAACACATGAAAAATACAGGCCAGTCAG
 GACCAGGGCTCCCTGCTTCCCCTGGCTGTGACCCCGTACCTCCATGTACCC
 GGCAGCCGTGCCCATGCAACATCACTATCTGAAAGGGAGAAGGGTACCGCGGAG
 ATCGAGGCCTCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCCAGGGCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCCGGAGAAGCCATGCACAGCAACCAACTACTACCAAGACGGTATCTCG
 ACACGGAGTCGTGAACCTCTACGACCACTTCAACATGTTCACCGCAAGTTCTACTGCTAC
 GTGCCCGGCCTCTACTTCTCAGCCTCAACGTGCACACCTGGAACCAAGAGGAGACCTACCT
 GCACATCATGAAGAACGAGGAGGAGGTGGTATCTTGTGCGCAGGTGGGAGCGCAGCA
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCAGAGCAGGACCGAGGTGTGGTACGCC
 TACAAGGGCGAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG
 TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGCCACCTCCTTCCTCGCC
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTTCCCCGATCCCTGGACTCCGACTC
 CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAGCGATCGGTGCTCC
 CAGATCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAAGGGGGCACCCGC
 GAGAACCCCTCTGGGACCTTCCGCAGGCCCTCTGCACACATCCTCAAGTGACCCGCACGGC
 GAGACGCCGGTGGCGCAGGGCGTCCCAGGGTGCAGGCCACCGGGCTCAGTCCTGGAAATA
 ATTAGGCAAATTCTAAAGGTCTAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
 TTGTTATTTGTCTTCCAGCCAGCCTGCTGGCTCCAAAGAGAGAGGGCTTTCAAGTTGAG
 ACTCTGCTTAAGAGAACATCCAAGTTAAAGCTCTGGGTCAAGGGAGGGCCGGGGCAGG
 AAACACTCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTGAGGGATAGGTGGACC
 CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGT
 GATGGGGCTGGGCCCCAGGGCTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTGGC
 TCCAGGGTGGTAGAACGAGCCGAAGGGCTCCTGACAGTGGCAGGGACCCCTGGTCCCCA
 GGCCTGCAGATGTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCCTGTGCCACCCAGGCCCTGGGGGTGGCTCCATGCCACCCCTGGCATCGGCT
 TTCTGTGCCGCCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGCCTTGGCTTCTGTTTT
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGCTAAGCATCACCGCTT
 CCACGTGTGTTGTTGGCTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTTCACTGCC
 CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAG
 CTGGAGGGCTAGAAAGCTCCGCTGTGTTCTCAGGCTCTGTGAGCCTCAGTCCTG
 AGACCAAGAGTCAGAGGAAGTACACGTCCAATCACCGTGTCAAGGATTCACTCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
 GTGTCTCCACGGTGCCTCGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC
 ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC
 CCCAAACCCCGCTGCCCTCTTCCCTCCCCCATCCCCACCTGGTTTGACTAATCCTGC
 TTCCCTCTCTGGGCTGGCTGCCGGATCTGGGTCCCTAAGTCCCTCTTTAAAGAACTT
 CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGCAGGCCACACTC
 GCTGCTTAAGCTCCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

TOP SECRET - SECURITY INFORMATION

APPROVED BY	O. G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

APPROVED BY DRAFTSMAN	O. G. FIG. CLASS SUBCLASS
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FIGURE 31

GCGGAGCATCCGCTCGGGCCTCGCCGAGACCCCCCGCGGATTGCCGGCCTTCCCGGG
 GCGCAGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGCGCGGGCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTAAAGCAAACATAAGACCAAGGGAGGATTAT
 CCTTGACCTTGAAGACAAAACATAACTGAAATTAAAATGTTCTCGGGGAGAAGGGAG
 CTTGACTTACACTTGTAATAATTGCTCCTGACACTAAGGCTGCTGCTAGTCAGAATT
 GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCGTATATACTCAACTCAAGAAGACTGCATTAATTCTGCTGTTAAC
 AAAAAACATATCAGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA
 GACAACCCAACGTACCTATTTCTGTCCTAACGAGGAAGCCTGTCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGACCAGAAATTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCAATTTCACAAGCAGTCACCCCC
 TAGCCCACATCACACAGATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAGATGGATGAAGCAAGTCCCCA
 GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCA
 CATACCCACCTCGCTACTCCAAAGCCGCCACCCCTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCCCTCATTTCTACAGTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTAGA
 AACCATACGTTACAGAAATCTCAAACTTAACATTGAACACAGGAATGTGTATAACCTA
 CTGCACTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCCAGGGCAGTGTCCAGAAAATCAGTACGGCTTCC
 ATTTGAAAATGGCTTCTATCGGGTCCCTGCTTTGGTGTCTGTCCTGGTGTAGGCC
 TCGTCCTCCTGGGTAGAATCCTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTGATCAATGGATCTATGGACATTAAGGATGGAACCTGGGTCTCTTAATTCTATT
 TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTTGCTAGCTTAGCAGGAGGTTG
 TATTGAAAGACAGGAAATGCCCTCTGCTTCTTCTTCTTGGAGACAGAGCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGATCTGGCTCTCACCGAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTAAGTATCTGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTGTATTTAGTAGAGACGGGTTCACCATGTTGGTCAGGCTG
 GTCTCAAACCTGACCTAGTGATCCACCCCTCTCGGCCTCCAAAGTGTGGATTACAGG
 CATGAGGCCACCACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTGGTAATCTGCTCTAAATATTAGCTAAAACAAAGCTCT
 ATGTAAGTAATAAAAGTATAATTGCCATATAAAATTCAAACGGCTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCACATTCTGGTCCAGATAAAATCAAC
 TGTTATATCAATTCTAATGGATTGCTTTCTTTATGGATTCTTAAACTTATT
 CCAGATGTTAGGTTCCAATTAAATATTGAATAATCTTTGTTACTCAA

APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGLTYTLVIICFLRLSASQNCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPPTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTAWEGRREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

APPROVED BY	O G. FIG.
DRAFTSMAN	CLASS SUBCLASS

FIGURE 33

CGGGCACCTGGAAG**ATG**CGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATGGGGAGAGGCCTGCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA
ATGTGACAGCAACACGATTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAAGAGTGCTGCTCCAAAATCCCTGCTCTTATGGTACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAACATGCCATAGAACGACTTGGAAAGTAAAGAAATCAGGAACA
TGAAATTCAAGGTCTAGCTGGTATTATTGCAGCAAAAGGCTTGGAACTCCCTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAG**TGA**ACTGCAGGGTCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAAATCGCTCAAGAACATCTTATTGCTAAATCCAACA
GCCCATATTGATGAGTATTTGGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTATACCAAGTATTTATGTTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAA

SEARCHED INDEXED

APPROVED	U G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

FIGURE 34

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777  
><subunit 1 of 1, 235 aa, 1 stop  
><MW: 25982, pI: 9.09, NX(S/T): 2  
MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMDYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125